## SEQUENCE LISTING

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<110>
       Ben-Yehuda, Dina
       Ashhab, Yaqoub
       Nachmias, Boaz
       Livin-derived peptides, compositions and uses thereof
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Glu Gly Ala Gly Ala Thr Leu Ser Arg Gly Pro Ala Phe Pro Gly Met 20 25 30
Gly Ser Glu Glu Leu Arg Leu Ala Ser Phe Tyr Asp Trp Pro Leu Thr
Ala Glu Val Pro Pro Glu Leu Leu Ala Ala Gly Phe Phe His Thr 50 55 60
Gly His Gln Asp Lys Val Arg Cys Phe Phe Cys Tyr Gly Gly Leu Gln 65 70 75 80
Ser Trp Lys Arg Gly Asp Asp Pro Trp Thr Glu His Ala Lys Trp Phe
85 90 95
Pro Ser Cys Gln Phe Leu Leu Arg Ser Lys Gly Arg Asp Phe Val His
Ser Val Gln Glu Thr His Ser Gln Leu Leu Gly Ser Trp Asp Pro Trp
                                                   125
Glu Glu Pro Glu Asp Ala Ala Pro Val Ala Pro Ser Val Pro Ala Ser
    130
Gly Tyr Pro Glu Leu Pro Thr Pro Arg Arg Glu Val Gln Ser Glu Ser
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Ala Gln Glu Pro Gly Gly Val Ser Pro Ala Glu Ala Gln Arg Ala Trp

Trp Val Leu Glu Pro Pro Gly Ala Arg Asp Val Glu Ala Gln Leu Arg 185

Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys Leu Asp Arg Ala Val Ser Ile Val Phe Val Pro Cys Gly His Leu Val Cys Ala Glu Cys Ala Glu Cys Ala Pro Gly Leu Gln Leu Cys Pro Ile Cys Arg Ala Pro Val Arg Ser Arg 230

Val Arg Thr Phe Leu Ser 245

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Glu Glu Pro Glu Asp Ala Ala Pro Val Ala Pro Ser Val Pro Ala Ser Gly Tyr Pro Glu Leu Pro Thr Pro Arg Arg Glu Val Gln Ser Glu Ser 145

Ala Gln Glu Pro Gly Ala Arg Asp Val Glu Ala Gln Leu Arg Arg Leu 175

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Gln Glu Glu Arg Thr Cys Lys Val Cys Leu Asp Arg Ala Val Ser Ile
180 185 190
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Leu Gln Leu Cys Pro Ile Cys Arg Ala Pro Val Arg Ser Arg Val Arg
210 215 220
Thr Phe Leu Ser
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Ser His Trp Ala Ala Gly Asp Gly Pro Thr Gln Glu Arg Cys Gly Pro
20 25 30
Arg Ser Leu Gly Ser Pro Val Leu Gly Leu Asp Thr Cys Arg Ala Trp 35 40 45
Asp His Val Asp Gly Gln Ile Leu Gly Gln Leu Arg Pro Leu Thr Glu
Glu Glu Glu Glu Gly Ala Gly Ala Thr Leu Ser Arg Gly Pro Ala
65 70 75 80
Phe Pro Gly Met Gly Ser Glu Glu Leu Arg Leu Ala Ser Phe Tyr Asp
85 90 95
Trp Pro Leu Thr Ala Glu Val Pro Pro Glu Leu Leu Ala Ala Ala Gly
Phe Phe His Thr Gly His Gln Asp Lys Val Arg Cys Phe Phe Cys Tyr
115 120 125
Gly Gly Leu Gln Ser Trp Lys Arg Gly Asp Asp Pro Trp Thr Glu His 130 135 140
Ala Lys Trp Phe Pro Ser Cys Gln Phe Leu Leu Arg Ser Lys Gly Arg
                       150
Asp Phe Val His Ser Val Gln Glu Thr His Ser Gln Leu Leu Gly Ser
165 170 175
Trp Asp Pro Trp Glu Glu Pro Glu Asp Ala Ala Pro Val Ala Pro Ser
180 185 190
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Val Pro Ala Ser Gly Tyr Pro Glu Leu Pro Thr Pro Arg Arg Glu Val

195 200 205

Gln Ser Glu Ser Ala Gln Glu Pro Gly Gly Val Ser Pro Ala Glu Ala 210 215 220

Gln Arg Ala Trp Trp Val Leu Glu Pro Pro Gly Ala Arg Asp Val Glu 225 230 235 240

Ala Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys Leu 245 250 255

Asp Arg Ala Val Ser Ile Val Phe Val Pro Cys Gly His Leu Val Cys 260 265 270

Ala Glu Cys Ala Pro Gly Leu Gln Leu Cys Pro Ile Cys Arg Ala Pro 275 280 285

Val Arg Ser Arg Val Arg Thr Phe Leu Ser 290 295

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Met Gly Pro Lys Asp Ser Ala Lys Cys Leu His Arg Gly Pro Gln Pro 1 5 10 15

Ser His Trp Ala Ala Gly Asp Gly Pro Thr Gln Glu Arg Cys Gly Pro 20 25 30

Arg Ser Leu Gly Ser Pro Val Leu Gly Leu Asp Thr Cys Arg Ala Trp 35 40 45

Asp His Val Asp Gly Gln Ile Leu Gly Gln Leu Arg Pro Leu Thr Glu 50 60

Glu Glu Glu Glu Gly Ala Gly Ala Thr Leu Ser Arg Gly Pro Ala 65 70 75 80

Phe Pro Gly Met Gly Ser Glu Glu Leu Arg Leu Ala Ser Phe Tyr Asp 85 90 95

Trp Pro Leu Thr Ala Glu Val Pro Pro Glu Leu Leu Ala Ala Ala Gly 100 105 110

Phe Phe His Thr Gly His Gln Asp Lys Val Arg Cys Phe Phe Cys Tyr 115 120 125

Gly Gly Leu Gln Ser Trp Lys Arg Gly Asp Asp Pro Trp Thr Glu His 130 135 140

Ala Lys Trp Phe Pro Ser Cys Gln Phe Leu Leu Arg Ser Lys Gly Arg 145 150 155 160

| Asp Ph  | e Val   | His        | ser<br>165 | Val        | Gln        | Glu        | Thr        | His<br>170 | Ser        | Gln        | Leu        | Leu        | Gly<br>175 | Ser        |  |  |
|---|---|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|--|--|
| Trp As  | p Pro   | Trp<br>180 | G∃u        | Glu        | Pro        | Glu        | Asp<br>185 | Ala        | Ala        | Pro        | Val        | Ala<br>190 | Pro        | Ser        |  |  |
| Val Pr  | o Ala<br>195  | ser        | Gly        | туr        | Pro        | G]u<br>200 | Leu        | Pro        | Thr        | Pro        | Arg<br>205 | Arg        | Glu        | val        |  |  |
| Gln Se<br>21  |   | Ser        | Ala        | Gln        | G]u<br>215 | Pro        | Gly        | Ala        | Arg        | Asp<br>220 | val        | Glu        | Ala        | Gln        |  |  |
| Leu Ar<br>225   | g Arg   | Leu        | Gln        | Glu<br>230 | Glu        | Arg        | Thr        | Cys        | Lys<br>235 | Val        | Cys        | Leu        | Asp        | Arg<br>240 |  |  |
| Ala Va  | l Ser   | Ile        | val<br>245 | Phe        | val        | Pro        | Cys        | Gly<br>250 | His        | Leu        | Val        | Cys        | A1a<br>255 | Glu        |  |  |
| Cys Al  | a Pro   | Gly<br>260 | Leu        | Gln        | Leu        | Cys        | Pro<br>265 | Ile        | Cys        | Arg        | Ala        | Pro<br>270 | val        | Arg        |  |  |
| Ser Ar  | g Val<br>275  | Arg        | Thr        | Phe        | Leu        | Ser<br>280 |            |            |            |            |            |            |            |            |  |  |
| <210><br><211><br><212><br><213>                      | 5<br>27<br>DNA<br>Arti                              | ficia      | al Se      | equer      | ıce        |            |            |            |            |            |            |            |            |            |  |  |
| <220> <223> Primer for site-directed mutagenesis      |   |            |            |            |            |            |            |            |            |            |            |            |            |            |  |  |
| <400> 5<br>ggggaattct ggtcagagcc agtgttc              |   |            |            |            |            |            |            |            |            |            | 27         |            |            |            |  |  |
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| <400> 6<br>gggggatccg gagcccactc tgca                 |   |            |            |            |            |            |            |            |            |            | 24         |            |            |            |  |  |
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| <220><br><223> Mega-primer to introduce mutation D52E |   |            |            |            |            |            |            |            |            |            |            |            |            |            |  |  |
| <400> 7<br>cgtggaaggg cagatcct                        |   |            |            |            |            |            |            |            |            |            | 18         |            |            |            |  |  |
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| <212><br><213>                   | DNA<br>Artificial Sequence                   |    |
|----------------------------------|--|----|
| <220><br><223>                   | Mega-primer to introduce mutation D238E      |    |
| <400><br>ccaggg                  | 8<br>aagt agaggcgca                          | 19 |
| <210><br><211><br><212><br><213> |  |    |
| <220><br><223>                   | Primer to construct cleavage fragment        |    |
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| <400><br>ggcaaa                  | 11<br>gctt ctaggacagg aaggtgc                | 27 |